RAW SEQUENCE LISTING

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Application Serial Number: _10/538,198_

Source: _PCT_

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RAW SEQUENCE LISTING   DATE: 02/16/2006
PATENT APPLICATION: US/10/538,198   TIME: 13:05:21

Input Set : **A:\2005-12-23 0933-0247PUS1.ST25.txt**
Output Set: **N:\CRF4\02162006\J538198.raw**

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 3 <110> APPLICANT: SALONEN, Jukka T.
 4         PIRSKANEN, Mia
 5         TUOMAINEN, Tomi-Pekka
 6         YUNUS, Faisel
 8 <120> TITLE OF INVENTION: METHOD AND KIT FOR DETECTING A RISK OF DIABETES OR A
METABOLIC SYNDROME
10 <130> FILE REFERENCE: 0933-0247PUS1
12 <140> CURRENT APPLICATION NUMBER: US 10/538,198
13 <141> CURRENT FILING DATE: 2005-06-09
15 <150> PRIOR APPLICATION NUMBER: PCT/FI03/00946
16 <151> PRIOR FILING DATE: 2003-12-11
18 <150> PRIOR APPLICATION NUMBER: FI 20022178
19 <151> PRIOR FILING DATE: 2002-12-11
21 <160> NUMBER OF SEQ ID NOS: 6
23 <170> SOFTWARE: PatentIn version 3.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1344
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)..(1341)
33 <223> OTHER INFORMATION: ADRA2B variant type sequence
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40 gcg gcc atc acc ttc ctc att ctc ttt acc atc ttc ggc aac gct ctg      96
41 Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu
42              20                  25                  30
44 gtc atc ctg gct gtg ttg acc agc cgc tcg ctg cgc gcc cct cag aac     144
45 Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
46          35                  40                  45
48 ctg ttc ctg gtg tcg ctg gcc gcc gcc gac atc ctg gtg gcc acg ctc     192
49 Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
50      50                  55                  60
52 atc atc cct ttc tcg ctg gcc aac gag ctg ctg ggc tac tgg tac ttc     240
53 Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
54 65                  70                  75                  80
56 cgg cgc acg tgg tgc gag gtg tac ctg gcg ctc gac gtg ctc ttc tgc     288
57 Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
58                  85                  90                  95
60 acc tcg tcc atc gtg cac ctg tgc gcc atc agc ctg gac cgc tac tgg     336
61 Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
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64 gcc gtg agc cgc gcg ctg gag tac aac tcc aag cgc acc ccg cgc cgc   384
65 Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg
66           115              120              125
68 atc aag tgc atc atc ctc act gtg tgg ctc atc gcc gcc gtc atc tcg   432
69 Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser
70      130              135              140
72 ctg ccg ccc ctc atc tac aag ggc gac cag ggc ccc cag ccg cgc ggg   480
73 Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly
74 145              150              155              160
76 cgc ccc cag tgc aag ctc aac cag gag gcc tgg tac atc ctg gcc tcc   528
77 Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser
78           165              170              175
80 agc atc gga tct ttc ttt gct cct tgc ctc atc atg atc ctt gtc tac   576
81 Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr
82           180              185              190
84 ctg cgc atc tac ctg atc gcc aaa cgc agc aac cgc aga ggt ccc agg   624
85 Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg
86           195              200              205
88 gcc aag ggg ggg cct ggg cag ggt gag tcc aag cag ccc cga ccc gac   672
89 Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp
90      210              215              220
92 cat ggt ggg gct ttg gcc tca gcc aaa ctg cca gcc ctg gcc tct gtg   720
93 His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val
94 225              230              235              240
96 gct tct gcc aga gag gtc aac gga cac tcg aag tcc act ggg gag aag   768
97 Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys
98           245              250              255
100 gag gag ggg gag acc cct gaa gat act ggg acc cgg gcc ttg cca ccc   816
101 Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro
102          260              265              270
104 agt tgg gct gcc ctt ccc aac tca ggc cag ggc cag aag gag ggt gtt   864
105 Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val
106          275              280              285
108 tgt ggg gca tct cca gag gat gaa gct gaa gag gag gaa gag gag gag   912
109 Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Glu
110     290              295              300
112 gag gag tgt gaa ccc cag gca gtg cca gtg tct ccg gcc tca gct tgc   960
113 Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala Ser Ala Cys
114 305              310              315              320
116 agc ccc ccg ctg cag cag cca cag ggc tcc cgg gtg ctg gcc acc cta   1008
117 Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu Ala Thr Leu
118               325              330              335
120 cgt ggc cag gtg ctc ctg ggc agg ggc gtg ggt gct ata ggt ggg cag   1056
121 Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile Gly Gly Gln
122          340              345              350
124 tgg tgg cgt cga agg gcg cac gtg acc cgg gag aag cgc ttc acc ttc   1104
125 Trp Trp Arg Arg Arg Ala His Val Thr Arg Glu Lys Arg Phe Thr Phe
126          355              360              365
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128 gtg ctg gct gtg gtc att ggc gtt ttt gtg ctc tgc tgg ttc ccc ttc   1152
129 Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp Phe Pro Phe
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132 ttc ttc agc tac agc ctg ggc gcc atc tgc ccg aag cac tgc aag gtg   1200
133 Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His Cys Lys Val
134 385             390             395             400
136 ccc cat ggc ctc ttc cag ttc ttc ttc tgg atc ggc tac tgc aac agc   1248
137 Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr Cys Asn Ser
138             405             410             415
140 tca ctg aac cct gtt atc tac acc atc ttc aac cag gac ttc cgc cgt   1296
141 Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp Phe Arg Arg
142             420             425             430
144 gcc ttc cgg agg atc ctg tgc cgc ccg tgg acc cag acg gcc tgg tga   1344
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150 <211> LENGTH: 447
151 <212> TYPE: PRT
152 <213> ORGANISM: Homo sapiens
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161             20              25              30
164 Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
165             35              40              45
168 Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
169     50              55              60
172 Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
173 65              70              75              80
176 Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys
177             85              90              95
180 Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
181             100             105             110
184 Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg
185             115             120             125
188 Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser
189     130             135             140
192 Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly
193 145             150             155             160
196 Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser
197             165             170             175
200 Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr
201             180             185             190
204 Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg
205             195             200             205
208 Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp
209     210             215             220
212 His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val
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216 Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys
217                    245                    250                    255
220 Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro
221                    260                    265                    270
224 Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val
225           275                    280                    285
228 Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Glu
229      290                    295                    300
232 Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala Ser Ala Cys
233 305                    310                    315                    320
236 Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu Ala Thr Leu
237                    325                    330                    335
240 Arg Gly Gln Val Leu Leu Gly Arg Gly Val Gly Ala Ile Gly Gly Gln
241                    340                    345                    350
244 Trp Trp Arg Arg Arg Ala His Val Thr Arg Glu Lys Arg Phe Thr Phe
245           355                    360                    365
248 Val Leu Ala Val Val Ile Gly Val Phe Val Leu Cys Trp Phe Pro Phe
249    370                    375                    380
252 Phe Phe Ser Tyr Ser Leu Gly Ala Ile Cys Pro Lys His Cys Lys Val
253 385                    390                    395                    400
256 Pro His Gly Leu Phe Gln Phe Phe Phe Trp Ile Gly Tyr Cys Asn Ser
257                    405                    410                    415
260 Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Gln Asp Phe Arg Arg
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269 <211> LENGTH: 1353
270 <212> TYPE: DNA
271 <213> ORGANISM: Homo sapiens
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274 <221> NAME/KEY: CDS
275 <222> LOCATION: (1)..(1350)
276 <223> OTHER INFORMATION: ADRA2B wild type sequence
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283 gcg gcc atc acc ttc ctc att ctc ttt acc atc ttc ggc aac gct ctg    96
284 Ala Ala Ile Thr Phe Leu Ile Leu Phe Thr Ile Phe Gly Asn Ala Leu
285           20                  25                  30
287 gtc atc ctg gct gtg ttg acc agc cgc tcg ctg cgc gcc cct cag aac   144
288 Val Ile Leu Ala Val Leu Thr Ser Arg Ser Leu Arg Ala Pro Gln Asn
289           35                  40                  45
291 ctg ttc ctg gtg tcg ctg gcc gcc gcc gac atc ctg gtg gcc acg ctc   192
292 Leu Phe Leu Val Ser Leu Ala Ala Ala Asp Ile Leu Val Ala Thr Leu
293      50                  55                  60
295 atc atc cct ttc tcg ctg gcc aac gag ctg ctg ggc tac tgg tac ttc   240
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296 Ile Ile Pro Phe Ser Leu Ala Asn Glu Leu Leu Gly Tyr Trp Tyr Phe
297 65                  70                  75                  80
299 cgg cgc acg tgg tgc gag gtg tac ctg gcg ctc gac gtg ctc ttc tgc      288
300 Arg Arg Thr Trp Cys Glu Val Tyr Leu Ala Leu Asp Val Leu Phe Cys      .
301                  85                  90                  95
303 acc tcg tcc atc gtg cac ctg tgc gcc atc agc ctg gac cgc tac tgg      336
304 Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Trp
305                  100                 105                 110
307 gcc gtg agc cgc gcg ctg gag tac aac tcc aag cgc acc ccg cgc cgc      384
308 Ala Val Ser Arg Ala Leu Glu Tyr Asn Ser Lys Arg Thr Pro Arg Arg
309                  115                 120                 125
311 atc aag tgc atc atc ctc act gtg tgg ctc atc gcc gcc gtc atc tcg      432
312 Ile Lys Cys Ile Ile Leu Thr Val Trp Leu Ile Ala Ala Val Ile Ser
313      130                 135                 140
315 ctg ccg ccc ctc atc tac aag ggc gac cag ggc ccc cag ccg cgc ggg      480
316 Leu Pro Pro Leu Ile Tyr Lys Gly Asp Gln Gly Pro Gln Pro Arg Gly
317 145                 150                 155                 160
319 cgc ccc cag tgc aag ctc aac cag gag gcc tgg tac atc ctg gcc tcc      528
320 Arg Pro Gln Cys Lys Leu Asn Gln Glu Ala Trp Tyr Ile Leu Ala Ser
321                  165                 170                 175
323 agc atc gga tct ttc ttt gct cct tgc ctc atc atg atc ctt gtc tac      576
324 Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met Ile Leu Val Tyr
325                  180                 185                 190
327 ctg cgc atc tac ctg atc gcc aaa cgc agc aac cgc aga ggt ccc agg      624
328 Leu Arg Ile Tyr Leu Ile Ala Lys Arg Ser Asn Arg Arg Gly Pro Arg
329      195                 200                 205
331 gcc aag ggg ggg cct ggg cag ggt gag tcc aag cag ccc cga ccc gac      672
332 Ala Lys Gly Gly Pro Gly Gln Gly Glu Ser Lys Gln Pro Arg Pro Asp
333      210                 215                 220
335 cat ggt ggg gct ttg gcc tca gcc aaa ctg cca gcc ctg gcc tct gtg      720
336 His Gly Gly Ala Leu Ala Ser Ala Lys Leu Pro Ala Leu Ala Ser Val
337 225                 230                 235                 240
339 gct tct gcc aga gag gtc aac gga cac tcg aag tcc act ggg gag aag      768
340 Ala Ser Ala Arg Glu Val Asn Gly His Ser Lys Ser Thr Gly Glu Lys
341                  245                 250                 255
343 gag gag ggg gag acc cct gaa gat act ggg acc cgg gcc ttg cca ccc      816
344 Glu Glu Gly Glu Thr Pro Glu Asp Thr Gly Thr Arg Ala Leu Pro Pro
345                  260                 265                 270
347 agt tgg gct gcc ctt ccc aac tca ggc cag ggc cag aag gag ggt gtt      864
348 Ser Trp Ala Ala Leu Pro Asn Ser Gly Gln Gly Gln Lys Glu Gly Val
349      275                 280                 285
351 tgt ggg gca tct cca gag gat gaa gct gaa gag gag gaa gag gag gag      912
352 Cys Gly Ala Ser Pro Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Glu
353      290                 295                 300
355 gag gag gag gaa gag tgt gaa ccc cag gca gtg cca gtg tct ccg gcc      960
356 Glu Glu Glu Glu Glu Cys Glu Pro Gln Ala Val Pro Val Ser Pro Ala
357 305                 310                 315                 320
359 tca gct tgc agc ccc ccg ctg cag cag cca cag ggc tcc cgg gtg ctg      1008
360 Ser Ala Cys Ser Pro Pro Leu Gln Gln Pro Gln Gly Ser Arg Val Leu
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VERIFICATION SUMMARY
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